

## AMENDMENTS TO THE SPECIFICATION

Amend the paragraph on page 11, lines 3 through 17 as follows:

The Expect value is used as a convenient way to create a significance threshold for reporting results. The default value used for blasting is typically set to 0.0001. In BLAST 2.0, the Expect value is also used instead of the P value (probability) to report the significance of matches. For example, an E value of one assigned to a hit can be interpreted as meaning that in a database of the current size one might expect to see one match with a similar score simply by chance. An E value of zero means that one would not expect to see any matches with a similar score simply by chance. See, e.g., ~~http://www.ncbi.nlm.nih.gov/Education/BLASTinfo/~~. Occasionally, a string of X's or N's will result from a BLAST search. This is a result of automatic filtering of the query for low-complexity sequence that is performed to prevent artifactual hits. The filter substitutes any low-complexity sequence that it finds with the letter "N" in nucleotide sequence (e.g., "NNNNNNNNNNNNNNNN") or the letter "X" in protein sequences (e.g., "XXXXXXXXXX"). Low-complexity regions can result in high scores that reflect compositional bias rather than significant position-by-position alignment. (Wootton and Federhen, Methods Enzymol 266:554-571, 1996).--

Amend the paragraph on page 21, line 48 through page 22, line 2 as follows:

--The presence of identifiable domains in NOV1, as well as all other NOVX proteins, was determined by searches using software algorithms such as PROSITE, DOMAIN, Blocks, Pfam, ProDomain, and Prints, and then determining the Interpro number by crossing the domain match (or numbers) using the Interpro website (~~http://www.ebi.ac.uk/interpro~~). DOMAIN results for NOV1 as disclosed in Tables 1I-IL, were collected from the Conserved Domain Database (CDD) with Reverse Position Specific BLAST analyses. This BLAST analysis software samples domains found in the Smart and Pfam collections. For Table 1E and all successive DOMAIN sequence alignments, fully conserved single residues are indicated by black shading or by the sign (!) and "strong" semi-conserved residues are indicated by grey shading or by the sign (+). The "strong" group of conserved amino acid residues may be any one of the following groups of amino acids: STA, NEQK, NHQK, NDEQ, QHRK, MILV, MILF, HY, FYW.--

Amend the paragraph starting on page 297, line 2 as follows:

Serial Analysis of Gene Expression, or SAGE, is an experimental technique designed to gain a quantitative measure of gene expression. The SAGE technique itself includes several steps utilizing molecular biological, DNA sequencing and bioinformatics techniques. These steps (reviewed in Adams MD, "Serial analysis of gene expression: ESTs get smaller." Bioessays. 18(4):261-2 (1996)) have been used to produce 9 or 10 base "tags", which are then, in some manner, assigned gene descriptions. For experimental reasons, these tags are immediately adjacent to the 3' end of the 3'-most NlaIII restriction site in cDNA sequences. The Cancer Genome Anatomy Project, or CGAP, is an NCI-initiated and sponsored project, which hopes to delineate the molecular fingerprint of the cancer cell. It has created a database of those cancer-related projects that used SAGE analysis in order to gain insight into the initiation and development of cancer in the human body. The SAGE expression profiles reported in this invention have been generated by first identifying the Unigene accession ID associated with the given MTC gene by querying the Unigene database at <http://www.ncbi.nlm.nih.gov/UniGene/>. This page has then a link to the SAGE : Gene to Tag mapping (<http://www.ncbi.nlm.nih.gov/SAGE/SAGEcid.cgi?cid='unigeneID'>), and then searching the SAGE database using the ID.--

Amend the paragraph starting on page 297, lines 18 through 22 as follows:

This generated the reports that are included in this application, which list the number of tags found for the given gene in a given sample along with the relative expression. This information is then used to understand whether the gene has a more general role in tumorigenesis and/or tumor progression. ~~A list of the SAGE libraries generated by CGAP and used in the analysis can be found at <http://www.ncbi.nlm.nih.gov/SAGE/sagelb.cgi>.~~